

IV. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2011 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11th International Wheat Genetics Symposium held in Brisbane, Australia, and the 2009 and 2010 Supplements (*Annual Wheat Newsletter* 55:256-278, 56:) are available from the Komugi (<http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp>) and GrainGenes (<http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/>) websites. The Wheat Gene Catalog is not included as part of the IWGS proceedings and, therefore, cannot be cited as part of them.

Morphological and Physiological Traits

Pre-harvest Sprouting

QTL

Argent (non-dormant, white seeded) / W98616 (dormant, white seeded): 90 DH lines: Strong QTL on chromosomes 1A, 3A, 4A, and 7A and weaker QTL on 2B, 5B, and 6B, all from W98616 {10740}.

XX.Embryo Lethality

XX.1.Embryo lethality in wheat x rye hybrids

The Chinese Spring (Imperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, and R7) produced hybrid seeds with different proportions of differentiated embryos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74–100% differentiated embryos {10748}. Crosses of R2 with the CS nulli-tetrasomics gave differentiated embryos only with N6AT6B and N6AT6D, indicating the presence of a complementary factor *Eml-A1* chromosome 6A {10748}.

39. Height

39.2. reduced Height : GA-sensitive

Rht14. 6AS {10767}. ma: *Rht14* – 11.7 cM – *Xbarc3-6A* {10767}.

Allelic with *Rht16* and *Rht18* {10767}.

Rht16. 6AS {10767}. ma: *Rht16* – 28.0 cM – *Xbarc3-6A* {10767}.

Allelic with *Rht14* and *Rht18* {10767}.

Rht18. 6AS {10767}. ma: *Rht18* – 25.1 cM – *Xbarc3-6A* {10767}.

Allelic with *Rht14* and *Rht16* {10767}.

43. Lack of Ligules

lg1., 2BS {10767}.

XX. Lesian Mimicry

Lesian mimics that resemble the responses of plants to infection by pathogens have occurred in many species ({10743} for examples).

lm {10743}. 1BL {10743}. **bin:** C1BL6-0.32 {10743}.
 v: Ning 7840 {10743}. **ma:** Proximal to *Xgwm264.I*-IB {10743}.

Lm was positively associated with *QLrpser.1BL* {10743}.

XX. Soft Glumes

sog. **bin:** C-2AS5-0.78. **dv:** Tm-9, a mutant of TA4342-96 {10769}.
 ma: *Xgwm71-2A* – 3.3 cM – *sog* – 3.5 cM – *Xbcd120-2A* {10769}.

Sog. **dv:** *T. monococcum* subsp. *aegilopoides* TA4342-96 {10769}.

Replace the previous entry regarding the relationship to Tenacious Glumes with: 'The Soft Glume locus is not an orthologue of Tenacious Glumes {10769}'.

69. Stem Solidness

Qsst.msub-3BL. Add following the current entry:
Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines {10730}.

71. Tenacious Glumes

Tg1. **bin:** 2BS-3 1.00-0.84.

Tg2. **v:** TA 3419 = Tetra Canthatch / *Ae. tauschii* var. *meyeri* TA1599 {10769}.
 ma: *Xgwm261/Xwmc503-2D* – 2.3 cM – *Tg2* – 5.9 cM – *Xfbc400-2D* {10769}.

Replace the note on the relationship with Soft Glumes with: 'The Tenacious Glume loci are not orthologues of the Soft Glume locus {10769}'.

75. Yield and Yield Components**75.1.2. 1,000-kernel weight**

TaGW2-6A {10781}. **ma:** *Xcf80-6AS.2* – 0.6 cM – *TaGW2-CAPS* – 0.5 cM – *Xbarc146-6A.1/Xwms132.4-6A* {10781}.

Based on its OsGW2 orthologue in rice, this gene was characterized and mapped as a CAPS marker in wheat {10781}. SNPs in the promoter region allowed distinction of two haplotypes. Hap-6A-A was mainly present in southern Chinese wheats; Hap6A-G was present in varieties from central and eastern Europe. On average, Hap-6A-A had 1,000-kernel weights more than 3 g higher than that of Hap-6A-G {10781}.

75.12. Spike number per plant

QSn.sdau-BL {10784}. **ma:** *Xwmc657-4B* – 4.6 cM – *QSn.sdau-4B* – 1.6 cM – *Xgwm495-4B* {10784}.
QSn.sdau-BL was resolved as a single gene in Line 05210/Laizhou 953 {10784}. It was associated with decreased spike length and grain number per spike.

Proteins**80.3. Endosperm storage proteins****80.3.1. Glutenins****80.3.1.1 Glu-1**

Glu-A1

Restore the following entries erroneously deleted in a previous update:

Glu-A1v {10327}. 2.1* {10327}. **v:** KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.

Wx-B1.

At the end of section add:

A dominant PCR marker for identifying heterozygotes at the *Wx-B1* locus is reported in {10732}.

77.5.8. Puroindolines and grain softness protein

Add note:

Lines possessing the alien-derived genes *Lr57* and *Yr40* lack puroindoline genes and, therefore, should be hard phenotypes {10770}.

77.5.12. Serine proteinase inhibitors

Serine proteinase inhibitors or serpins are salt soluble proteins (~43 kDa) representing about 4% of the total protein in wheat and barley endosperms. They may have a role in plant defense.

Srp-A1 {10754}. 5AL {10754}.

Srp-B1 {10754}. *Srp5B* {10754}. 5BL {10754}.

Srp-B1a {10754}. *Srp5Ba* {10754}.
v: Etawah {10755}; Federation {10755}; Frame {10755}; Pugsley {10754}; Stylet {10755}.

Srp-B1b {10754}. Null allele.
v: Correll {10755}; EGA Eagle Rock {10755}; Gladius 10755; Yitpi {10755}.

This allele reduced milling yield by 0.4% {10755}.

Srp-D1 {10754}. 5DL {10754}.

NEW SECTION: Abiotic Stress Responses

Dehydrin-response Element Binding Factors

DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers an orthologous *Dreb1* gene series was placed on chromosomes 3A, 3B, and 3D {10729}. SNPs in *Dreb-B1* permitted mapping in chromosome 3BL in the ITMI (Opata 85 / W7984) mapping population.

Dreb-B1 {10729}. 3BL {10729}.

ma: *Xmwg818-3B* – 27.3 cM – *Dreb1* – 11.2 cM – *Xfbb117-3B* {10729}.

Dreb-B1a [{10729}]. v: Opata 85 {10729}.

Dreb-B1b [{10729}]. v: W7984 {10729}.

Pathogenic Disease/Pest Reaction

79. Reaction to *Blumeria graminis* DC.**79.1. Designated genes for resistance**

Pm4d {10744}. 2AL {10744}. **bin:** 2AL1-0.85-1.00.

dv: *T. monococcum* Tm27 {10744}.

v: Tm27d2 = WW St 2022 / Tm27 // Amor = TRI 29584 {10744}.

ma: A 218-bp fragment was amplified with STS marker ResPm4 as were other *Pm4* alleles {10744}.

Pm17. **v:** McCormack {10758}; Tribute {10758}; TAM303 {10758}.

Pm41. **bin:** 0.63–1.00.

Pm44 {10790}. 3AS {10790}. **v:** Hombar {10790}.

ma: Flanked by SSR markers distally located in chromosome 3AS {10790}.

Pm45 {10791}. Pm57-6D {10790}. 6DS {10791}.

v1: Line NWG0099 {10791}.

v2: D57 {10791}.

ma: Close linkages are reported in the draft manuscript.

82. Reaction to *Fusarium graminearum*

82.2. Disease: Crown rot caused by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species.

'Cansas / Ritmo': After *QFHS.whs-5BL* add insert: '(remaned *Qfhs.lfl-1BL* in {10768})'. Then continue at end of the paragraph '*Qfhs.lfl-1BL* was verified in F4:7 lines and in detected Biscay, History and Pirat {10768}'.

'CS / CS (Sumai 3 7A)': *QFhb7AC*, nearest marker *Xwmc17-7A*, explained 22% of phenotypic variance for type-II and 24% of phenotypic variance for type-III resistance {10798}.

'Lang / *T. aestivum* subsp. *spelta* CSCR6': *Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495*; R^2 up to 0.49, validated in other crosses {10273}. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23 {10273}.

'Soissons (relatively resistant) / Orvantis (susceptible)': Add at end of paragraph: Increased susceptibility associated with the *Rht-D1b* allele was further confirmed in crosses of semi-dwarf cultivars Apachi, History, and Romanus {10793}.

83. Reaction to *Heterodera avenae* Woll.

QCRe.pau-1A {10749}. 1AS {10749}. dv: *T. monococcum* Tm 14087 *QCRe.pau-2A* {10749}.

ma: *QCRe.pau-1A* was mapped in a 3.6 cM interval in a *T. boeoticum* Tb 5088 / Tm 14087 RIL population and was flanked by *Xcfa2153-1A* and *BE444890* {10749}; $R^2 = 0.26$ {10749}.

QCRe.pau-1A was transferred to tetraploid and hexaploid lines {10749}.

QCRe.pau-2A {10749}. 2AS {10749}. dv: *T. monococcum* Tm 14087 *QCRe.pau-1A* {10749}.

ma: *QCRe.pau-2A* was mapped in a 4.00 cM interval flanked by *BE498358* and *Xwmc358-2A* {10749}; $R^2 = 0.13$ {10749}.

88. Reaction to *Meloidogyne* spp.

Root knot eelworm

Revise to:

Rkn1 [{632}].

Rkn {632}. 6D {10799}.

dv: *Ae. tauschii* G3489.

v: Prosquare, a synthetic hexaploid of 'Produra/*Ae. tauschii* G3489' {632}.

Rkn2 [{1621}].

3B{590}.

Derived from *Ae. peregrina* {1621}. *Rkn-mn1* {1621}.

v: X8 = 'CS/*Ae. peregrina* No. 1//Rescler/3/Lutin' {1620}; X35 {1620, 1621}.

ma: Co-segregation with RAPD *OpY16₁₀₆₅* and close linkage with several markers including *Est-B5* {0103}; converted to SCAR Y16 {10486}; may be the same as *CreY* (see reaction to *Heterodera avenae*) on chromosome 3S^v from *Ae. peregrina* translocated to 3BL {10800}.

Add:

Rkn3 {10801}.

Derived from *Ae. ventricosa*. 2NS translocation into 2AS {10801}.

v: VPM1, Lassik (PI 653535) {10801}.

ma: Resistances to *M. javanica* and *M. incognita* mapped to the 2NS translocation in BC_6F_3 near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation {10801}.

89. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

89.1. Genes for resistance

QTL

Add at the end of this section:

A summary of QTL analyses is provided in {10276}.

89.2. Sensitivity to SNB toxin

Insert at the beginning of this section:

A discussion on the origin and role of host-specific toxins is provided in {10276}.

Add:

- Tsn1.** **v:** Forno {10275}. **tv:** Add: Some *T. turgidum* subsp. *dicoccoides* accessions {10756}.
dv: Two *Ae. speltoides* accessions {10756}.
c: *Tsn1* has eight exons and a S/TPK-NBS-LRR structure; all three domains are required for function and the *Tsn1* protein does not interact directly with ToxA {10756}.
- tsn1.** **ma:** Add: This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B* {10274}.

Genotype list in {10274}.

- Snn1.** **bin:** 1BS.sat.18.
ma: *XksuD14.2-1BS* – 0.4 cM – *Snn1/XBE498831/XBF474204* – 0.4 cM – *Xpsp3000-1BS/XBE422980/XBE637568/ZBE605202* {10727}; *XksuD14.2* – 0.34 cM – *Snn1/XBE498831/XBF474204* – 0.12 cM – *XBF29322* – 0.04 cM – *Xpsp3000-1BS/XBE422980/XbE637568/XBF605202* {10727}.

- Snn2.** **ma:** *XTC253803* – 3.6 cM – *Snn2* – 0.4 cM – *Xcf2d-2D* {10274}.

- snn2.** **v:** Add: Atlas 66 {10274}; Cheyenne {10274}; Chinese Spring {10274}; Jagger {10274}; Opata 85 {10274}; Salamouni {10274}; TAM 105 {10274}.

- Snn3 {10728,10507}.** Sensitivity to *SnTox3* is dominant {10728}.

- 5BS {10728,10507}. **bin:** 5BS-6 {10507}.
v2: Grandin Snn2{10728,10507}.
ma: *Snn3* – 1.4 cM – *Xcf2d20-5BS* {10507}.

- snn3.** **v:** BR34 {10507}.

- Snn4 {10275}.** Sensitivity to *SnTox4* is dominant {10275}. **1AS {10275}.**
bin: 1AS3-0.86-1.00 {10275}. **v:** Arina {10275}.
ma: *XBG262267/XBG262975* – 0.9 cM – *Snn4* – 1.6 cM – *Xcf2d58.1-1AS* {10275}.

- snn4.** **v:** Forno {10275}.

QTL

'P91193D1 / P92201D5' RIL population: tested in the U.S.A. and Australia: *QSng.pur-2DL.1* from P91103D1, $R^2 = 0.123$ (Indiana) and 0.381 (South Perth); and *QSng.pur-2DL.2* from P92201D5, $R^2 = 0.069$ (Indiana) and 0.112 (South Perth) {10776}.

90. Reaction to *Puccinia graminis* Pers.

- Sr2.** **ma:** Add: Tightly linked CAPS marker csSr2 based on a SNP proved superior to *Xgwm533-3B* as a marker for *Sr2* {10786}.

- Sr13.** **bin:** 6AL-8. **tv:** Kronos {10777}; Medora {10777}; Sceptre {10777}.
ma: *CD926040* – *Sr13* – *BE471213* {10777}.

A gene in 'Khapstein/9*LMPG' and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However, the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance gene mapped in {10778} could not be *Sr13*.

- Sr22.** **bin:** 7AL-0.74-0.86. **v:** Recombinant line reported in {10772,10773}.
ma: Multiplex marker cssu22 based on STS markers derived from cloned fragment csIH81 was developed in {10772}. This marker gave positive results for *Sr22* in all recombinant lines including those reported in {10773}.

Sr38. Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.

Sr39. Add at the beginning of notes: Lines with shortened alien segments are reported in {10741}.

- Sr48.** **ma:** Replace the first sentence with: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.

- Sr50** [{10745}]. **SrR** {0377}. 1DS {10745}.
ad: CS + Imperial 1R {0377}. **v:** Line T6-1 AUS 91434 {10745}.
al: *S. cereale* cv. Imperial.
ma: Line T6-1 retains the rye marker AW2-5 {10745}.

In rye, *Sr50* may be allelic with *Sr31*; however, in wheat they can be regarded as separate loci. *Sr50* is located in a small interstitial segment not detected by GISH. Line T6-1 lacks the *Sec-1* allele from rye {10745}.

- Sr51** {10803}. Homoeologous group 3 {10803}; 3S^SS {10803}.
3A (T3AL·3S^SS) {10803}. **v:** TA5619 {10803}.
3B (T3BL·3S^SS) {10803}. **v:** TA5620 {10803}.
3D (T3DL·3S^SS) {10803}. **v:** TA5621 {10803}.
3D (T3DS-3S^SS·3S^LL) {10803}. **v:** TA5622 {10803}.
al: *Ae. searsii* TA2355 {10803}.
ma: 3^SS-specific markers are provided in {10803}.

- Sr52** {10774}. 6A (T6AS·6V#3L) {10774}.
v: TA5617 {10775}.
ma: 6V3- specific EST-STS markers are given in {10775}.

The seedling response conferred by *Sr52* is temperature-sensitive.

- Sr53** {10789}. Derived from *Ae. geniculata*. 5D {10789}.
Ti5DS-5DL-5M^gL-5DL {10789}. **v:** TA5630 (U6154-124) {10789}.
T5DL-5M^gL·5M^gS {10789}. **v:** TA5625 (U6200-64) {10789}.
T5DL-5M^gL·5M^gS {10789}. **v:** TA5643 (U6200-117) {10789}.
al: *Ae. geniculata* TA10437 {10789}.

The three translocation lines are re-engineered derivatives of TA5599 (5DL-5M^gL·5M^gS {10789}).

- SrCad** {10733}. 6DS {10733}.
v: AC Cadillac {10733}; AC Crystal {10733}; AC Foremost {10733}; AC Karma {10733}; AC Taber {10733}; AC 2000{10733}; Peace {10733}; 5700 {10733}.
ma: Lines with *Bt10* {10733}. *Xcf49-6D* – 7.7 cM – *SrCad* – 1.5 cM – *FSD_RSA/Bt10* – 14.1 cM – *Xbarc301-6D* – 8 cM – *Xbarc173-6D* {10733}; *Xcf49-6D* – 7.2 cM – *SrCad* – 1.8 cM – *FSD-RSA/Bt10* – 14 cM – *Xcf75-6D* {10733}.

SrR. Delete current listing.

91. Reaction to *Puccinia striiformis* Westend.

91.1. Designated genes for resistance to stripe rust

- Yr1.** **ma:** Replace the present entry with: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.

Lr17a. **ma:** Add: *Lr17a* – 3.7 cm – *Xbarc212-2a* {10795}.

Lr18. Add note: A resistance gene, *LrTt2*, in line 842-2 was located on chromosome 5BL in a similar region to *Lr18*. The claim that *Lr18* and *LrTt2* were different based on different low seedling infection types, but the genetic backgrounds were different {10752}.

Lr21. **v:** Lovitt {10766}; McKenzie {10766}

Add to notes: Further haplotype analyses are reported in {10766}.

Lr25. **i:** Tc+Lr25 *Lr48* {10738}.

Add note: *Lr25* is closely linked with *Lr48* {10738}.

Lr35. Add note at the end of section: Lines with shortened alien segments are reported in {10741}.

Lr37. Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.

Lr39. 2DS {add: , 10731}.

ma: Four markers, *Xbarc124-2D*, *Xgwm210-2D*, *Xgdm35-2D*, and *Xcf36-2D* were closely linked with the terminally located *Lr39* (formerly *Lr41*), but the gene order was inconsistent and no specific allele was associated with it {10731}.

Lr47. 7AS. **v:** Add: Bionta 2004 {10737}.

Lr48. , 4BS {10738}. **ma:** RAPD markers flanking *Lr48* at 2.7 and 8.6 cM are reported in {10738}.
Lr48 is closely linked with *Lr25* {10738}.

Lr53. **ma:** *Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcf6-6B* – 3.4 cM – *Xgwm50-6B* {10780}.

Lr53 was genetically independent of *Lr36* {10780}.

Lr57. **ma:** Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.

Lr59. Add note: Problems in recovering balanced recombinants are reported in {10762}.

Lr62 Add note: Associated with *Yr42* {10537}.

Lr67. **bin:** Distal to 0.56.

ma: add: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.

LrAlt {10739}. 2AS {10739}. **v:** *T. aestivum* subsp. *spelta* cv. Altgold {10739}.
ma: *LrAlt* – 1.8 cM – *Xbarc212-2A/Xwmc382-2A* – 2 cM – *Xgwm636-2A* {10739}.

LrWo {10747}. 5B {10747}. **tv:** Wollaroi AUS99174 {10747}.
ma: *Xgwm234-5B* – 7.2 cM – *LrWo* – 20.3 cM – *wPT-1420* {10747}.

The relationship of *LrWo* to *Lr52* was not established.

Add to the list: complex genotypes

Coker 9663 *Lr9 Lr10 Lr14a* {10742}

Pioneer 26R61 *Lr13 Lr14b Lr26* {10742}

Genotype lists: French cultivars {10792}. Add to European cultivars {....., 10794}.

92.3. QTL for reaction to *P. triticina*

Insert above *QLr.sfr-1B*:

QLr.pser.IBL {10743}. 1BL {10743}. **bin:** 1BL6-0.32 {10743}.
ma: Proximal to *Xgwm264.1-1BL* {10743}.

Associated with lm producing a lesian mimic phenotype in the absence of disease {10743}.

After the entry for ‘Avocet / Pavon’ add:

‘TA 4152-60 (MR) / ND495 (MR)’: DH population: Five QTL for APR were identified in the field, viz. *QLrfcu-3AL* ($R^2 = 0.18$), *QLrfcu-3BL* ($R^2 = 0.19$), *QLrfcu-5BL* ($R^2 = 0.07$), and *QLrfcu-6BL* ($R^2 = 0.12$) from TA 4152-60 and *QLrfcu-4DL* ($R^2 = 0.13$) from ND495 {10757}. The 3AL gene also conferred seedling resistance to some races and the 3BL gene conferred resistance to race MFPS {10757}.

Add:

Tetraploid wheat

Association mapping indicated genomic regions affecting leaf rust response in chromosomes 1A, 1B, 2A, 2B (*Lr13*, *Lr23* region), 3B, 5A, 5B, 6B, 7A, and 7B (see *Lr14*) {10736}.

93. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

93.1. Insensitivity to tan spot toxin

Tsn.

dv: Two *Ae. speltoides* accessions {10756}.

tv: Add: Some *T. turgidum* subsp. *dicoccoides* accessions{10756}.

c: *Tsn1* has eight exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA {10756}.

93.3. Resistance to tanspot

TsrAri {10765}.

Recessive.

3A {10765}.

v: Arina {10765}; Heines VII {10765}; Zenith {10765}.

Add: ‘Batavia (S) / Ernie (R)’: DH population tested over three years. Four (1A (Ernie), 7A, 2BS, 3BS (Batavia)), five (2BS, 5BL (E), 3D, 6A, 7D (B)), and four (2BS, 5BL (E) 1A, 6A (B)) QTL accounted for most of the variation in each year. The greatest effect across years was the QTL on chromosome 2BS ($R^2 = 0.382, 0.298$ and 0.362 , respectively). This QTL was validated in four additional populations {10782}.

‘Wangshuibai / Ning 7840’: RIL population: Race 1: *QTs.ksu-1AS*, $R^2 = 0.39$ (nearest marker *Xcfa2153-1A*) and *QTs.ksu-2BS*, $R^2 = 0.04$ (nearest marker *Xbarc2-2B*) {10753}.

94. Reaction to *Rhizoctonia* spp.

Cause of Rhizoctonia root rot.

Rot1 {10761}.

v: Scarlet-Rz1 {10761}.

Scarlet-Rz1 was produced by mutagenesis {10761}.

95. Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Gb2.

ma: Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.

Gb3.

v: TAM112 (10764). **al:** Insave rye.

Gb6.

v: N96L9970 {10764}.

ma: Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.

97. Reaction to *Tapesia yallundae* (Anomorph: *Pseudocerosporella herpotrichoides*)

Add at end of section:

QPch.jic-5A {10771}.

bin: 5AL-6; 0.68-0.78.

ma: Closely associated with *Xgwm639-5AL* {10771}.

98. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa***Bt10.****v:** Present in lines with *SrCad* {10733}.**QTL**

'Blizard (R) / 8405-JC3C (S)': DH population: Resistance and markers *Xgwm374-1BS*, *Xgwm364-1BS*, and *Xbarc128-1BS* were within a 3.9 cM interval {10783}.

102 .Reaction to Wheat Streak Mosaic Virus

Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosicella*. See: Resistance to colonization by *Eriophyes tulipae*. According to {10226} WSMV may also be seed-borne. At least some sources of resistance to WSMV are also effective against *Triticum* mosaic virus.

Update:

Wsm1 {379, 440}. Derived from *Th. intermedium*.4D = T4DL·4J^SS {391, 389}.**i:** Karl*4/CI 17884 = PI 583794 = KS93WGRC27{440}.**v:** CI 17766 = B-6-37-1 {391, 800, 1543}; CI 17884 {391} KS90H445 {391}; KS90H450 {391}; CI17883 {389}.**ad:** CI 17881; CI 17886{391}.**su:** 4J^SS (4A): CI 15092 {391}; 4J^SS (4D): CI 17882 and CI 17885 {391}.**ma:** *Wsm1* cosegregated with a STS amplified by the primer set STSJ15 {1456}.4D = T4DL·4DS-4J^SS {10788}.**v:** KS08WGGRG50 {10788}.4A {800} = T4AL·4J^SS {391}.6A = T6AS·4J^SL + T6AL·4J^SS {389}.

Wsm1 is located in 4J^SS (formerly 4Ai#2S). CI 17882, CI 17884, CI 17885, and KS90H445 also carry a 7S *Ae. speltoides* chromosome substituting for 7A (See Reaction to *Schizaphis graminum*).

Wsm1 also confers resistance to *Triticum* Mosaic Virus {10788}.

Wsm2.3BS (10802). **v:** CO960293-2 {10802}; Snowmass {10802}.**ma:** *Wsm2* – 5.2 cM – XSTS3B-55 {10802}; *Xbarc102-3B* – 1.6 cM – *Wsm2* {10802}.

Wsm2 confers resistance at temperatures below 19C {10802}.

Wsm3 {10775}.7B (T7BS·7S#3L) {10775}. **v:** TA5624 {10775}.**XX. Reaction to Wheat Yellow Mosaic Virus**

Vectored by *Polymyxa graminis*. MYMV is closely related to WSSMV, another bymovirus.

Ym1b {10750}.

2DL {10750}.

v: Ibis {10750}; Jagger {10750}; KS 831957 {10750}; Madsen {10750}; Yumechikara {10750}.**ma:** *Xwmc181-2D* – 12.4 cM – *Ym1b* – 2.0 cM – *Xcf16-2D* – 2.0 cM – *Xwmc41-2D* – 3.1 cM – *Xcf168-2D* {10750}.

The relationships of *Ym1b* to previously mapped gene in 2DL for resistance to WYMC and WSSMV in Yangfu 9311 {10258} and a Geneva derivative {0131} were not established.

References**Updates**

10375. Correct author name from 'Laur' to 'Kaur' and delete 'Draft manuscript'.
10507. Correct page numbers to 682-693.
10537. Marais F, Marais A, McCallum B & Pretorius Z 2009 Transfer of leaf rust and stripe rust resistance genes *Lr62* and *Yr42* from *Aegilops neglecta* Req. ex Bertol. to common wheat. Crop Science 49: 871-879.
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